

10/08/80 114

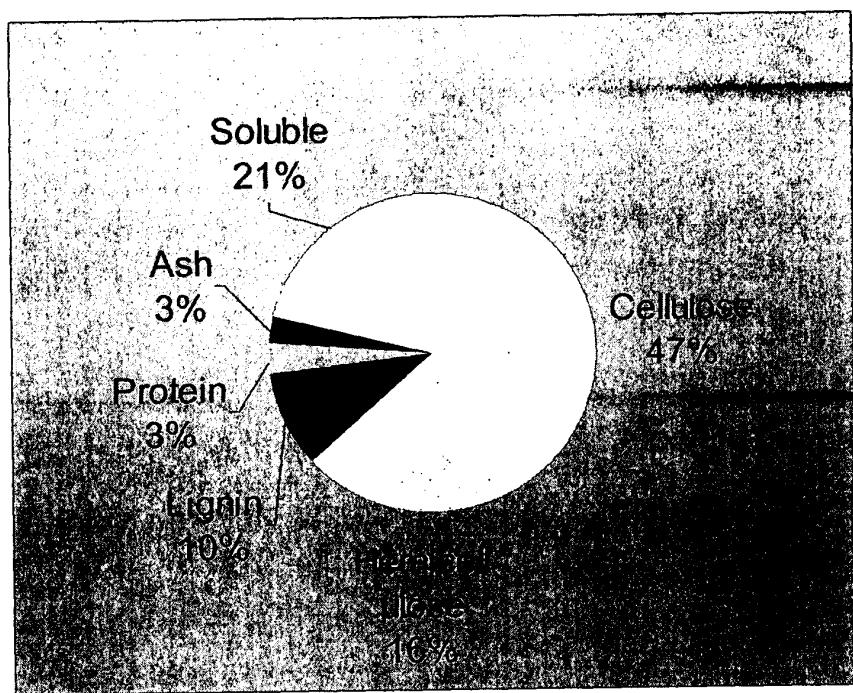


Figure 1.

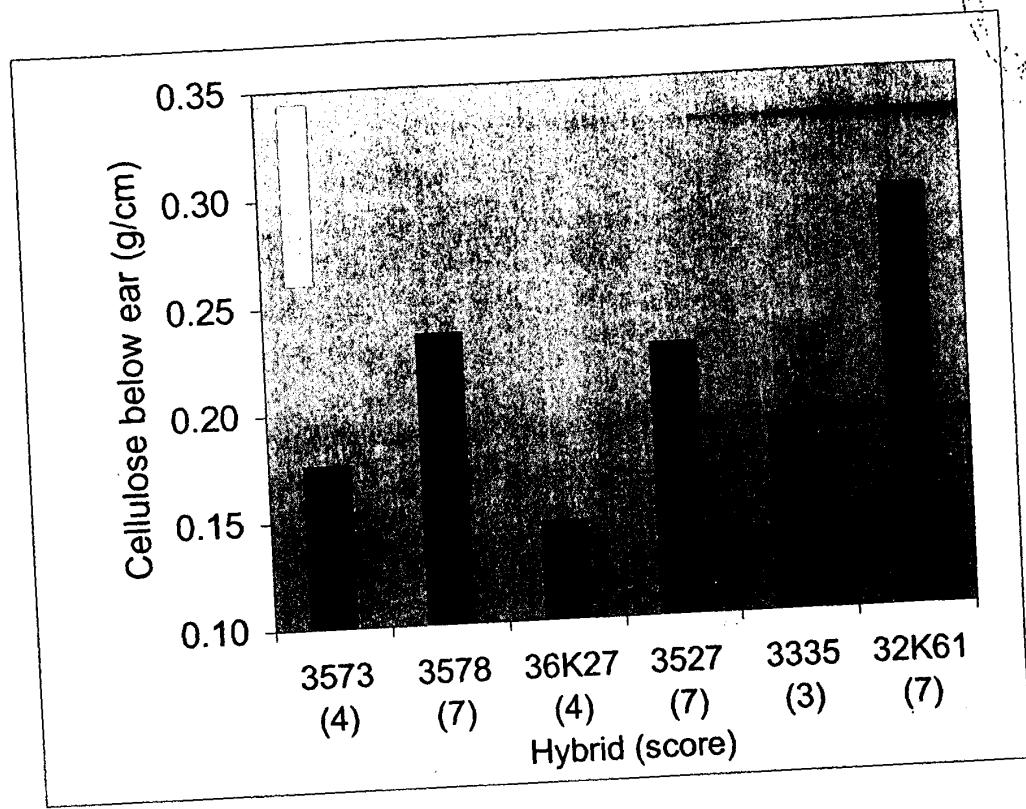


Figure 2

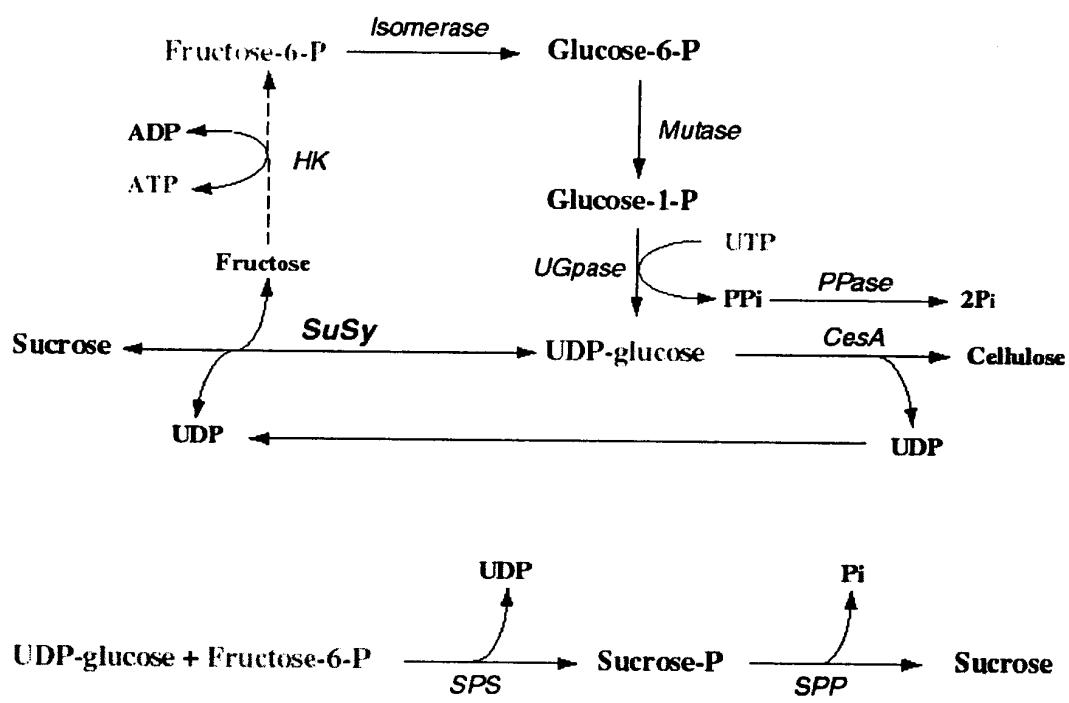


Figure 3.

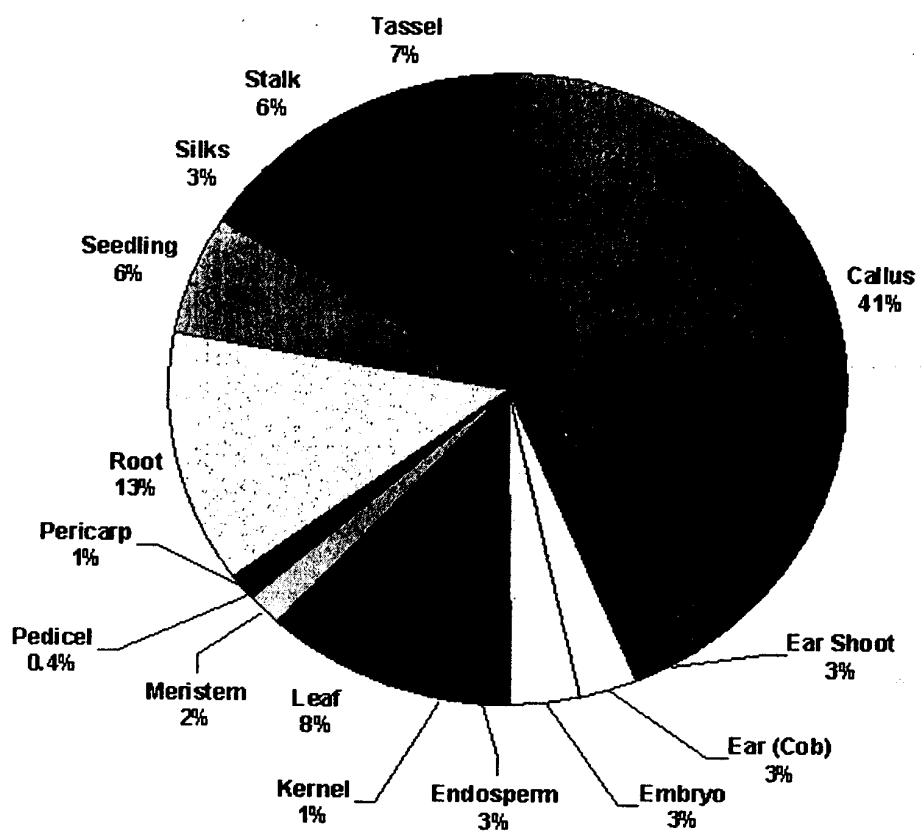


Figure 4.

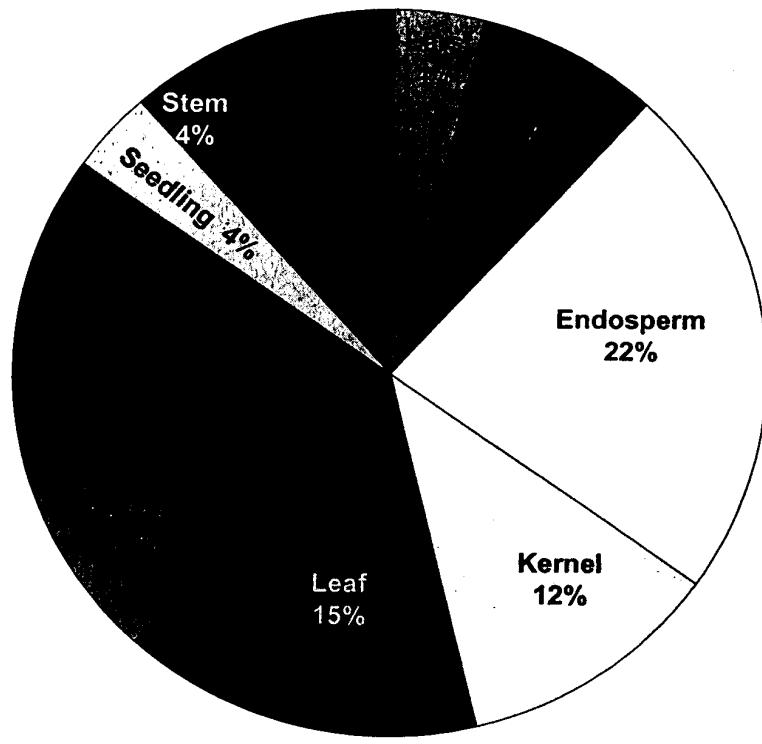


Figure 5

Allele 1: CACCCGG-mu-AGATTG

Allele 2: CACC-mu-CGGAGATTG



Figure 6.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellul s (% f structural dry matter)
<i>Sus-1</i> (WT)	63.2	25.2 +/-0.38	39.9
<i>sus-1</i> (mutant)	47.3	17.7 +/-0.34	37.4

Figure 7.

	1	50
Sh1	(1) -----MAAKLTRLHSRERIGATFSHPNELIALFSRYVHQSKGMLQPHQ	
Sus1	(1) MGEAGAGDRVLSRLHSRERIGDSLHAPNELVAVFIRLKNEKGMLQPHQ	
Sus3	(1) -----STHASGDRVEDTLHARNLVLLSKYVNKGKGTIOPPH	
Consensus	(1) LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLOPHQ	
	51	100
Sh1	(46) ILAEFD-AIPFDSDKE - KYAPPEDTIRAADEAIVLPPWALAIRPRPGVA	
Sus1	(51) IIAEYNNATPFAEREKLKDGAEDVLRRAAQEVLPFWALAIRPRPGVV	
Sus3	(40) ILDALDEVQGSGGRA-LAEGPFLDVURSAOAHVLDPEVIAVREPRPGW	
Consensus	(51) ILAEFD AI DADRE LKDGFEDVLRAAQEAIVLPPWALAIRPRPGVV	
	101	150
Sh1	(93) DYIVRVNVSELAVEELSVEYLSEYLAPEKEQLVDGQSNNSNFV	
Sus1	(101) EYVRVNVSELAVEELSPVPEYIQLKEQLYVEEGPNNFV	
Sus3	(89) EYVRVNVSELAVEELSPVQTYSEYIQLKEELVDGQHNDPV	
Consensus	(101) EYVRVNVSELAVEELSVEYL FKEQLVDGQ N NFVLELDFEFPNASFP	
	151	200
Sh1	(143) RPSLKSIGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNKG TMMLN	
Sus1	(151) RPSLKSIGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNKG TMMLN	
Sus3	(139) RPSLKSIGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNKG TMMLN	
Consensus	(151) RPSLKSIGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNKG TMMLN	
	201	250
Sh1	(193) QDRIQLRQSSRDPDSTLEAPDPOVTEENHR	
Sus1	(201) QDRIQLRQSSRDPDSTLEAPDPOVTEENHR	
Sus3	(189) QDRIQLRQSSRDPDSTLEAPDPOVTEENHR	
Consensus	(201) DRIQLS ALQSALRKAEHLSSLPADTPYSEF HRFQELGLEKGWGDATK	
	251	300
Sh1	(243) RVLTIHLLLLEAPDSTLEAPDPOVTEENHR	
Sus1	(251) RAQETIHLLEAPDSTLEAPDPOVTEENHR	
Sus3	(239) HVLEMIDTQDPTLEAPDSTLEAPDPOVTEENHR	
Consensus	(251) RVLTIHLLLLEAPDSTLEKFLGTPMIFNVVILSPHGYFAQANVLG	
	301	350
Sh1	(293) YPDGGQVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDA GT	
Sus1	(301) YPDGGQVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDA GT	
Sus3	(289) YPDGGQVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDA GT	
Consensus	(301) YPDGGQVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDA GT	
	351	400
Sh1	(343) TCGQRLEKVIGTEHTDLRVPFRNENGILRKWISRFDVWPYLETYEDVA	
Sus1	(351) TCGQRLEKVIGTEHTDLRVPFRNENGILRKWISRFDVWPYLETYEDVA	
Sus3	(339) SCDNORLERISGTOHTDLRVPFRNENGILRKWISRFDVWPYLETYEDVA	
Consensus	(351) TCGQRLEKVIGTEHTDLRVPFRNENGILRKWISRFDVWPYLETYEDVA	
	401	450
Sh1	(393) SEIMKEMOAKPDLIIGNYSDGNLVATLLAHKGTVQCTIALEKTKYEN	
Sus1	(401) HETAGELOANPDLIIGNYSDGNLVATLLAHKGTVQCTIALEKTKYEN	
Sus3	(389) GTEAAELOGTPDFIIGNYSDGNLVASLLSYKMGTQCTIALEKTKYED	
Consensus	(401) EIAAELQA PDLIIGNYSDGNLVASLLAHKGTVQCTIALEKTKYEN	
	451	500
Sh1	(443) SDIYLDKFDSQYHFSCQFTADLIAMNHDFIITSTFOEIAGSKDFTVGOYE	
Sus1	(451) SDIYWKKFEDHYHFSCQFTADLIAMNHDFIITSTFOEIAGSKDFTVGOYE	
Sus3	(439) SDIFWKNFDEKYHFSCQFTADLIAMNNADFIITSTFOEIAGSKDFTVGOYE	
Consensus	(451) SDIYWKKFDD YHFSCQFTADLIAMNHDFIITSTFOEIAGSKDFTVGOYE	
	501	550
Sh1	(493) SHIAFTLPGLYRVRVHGIDVFDPKFNI VSPGADMMSVYYPYTETDKRLTAFH	
Sus1	(501) SHMAFTMPGLYRVRVHGIDVFDPKFNI VSPGADLSIYFPYTESHKRLTLSH	
Sus3	(489) SHTAFTLPGLYRVRVHGIDVFDPKFNI VSPGADMMSIYFPHTEKAKRLTLSH	
Consensus	(501) SHIAFTLPGLYRVRVHGIDVFDPKFNI VSPGADMMSIYFPYTES KRLTLSH	

Figure 8a

	551		
Sh1	(543) PEIEELIYS D VENSEHKFV L KDKKKP II FSMARLDRVKNMTGLVEMYGKN	600	
Sus1	(551) PEIEELIYS Q TENTEHKFV L NDRNKP II FSMARLDRVKNLTGLVELYGRN		
Sus3	(539) GS IENI IDPEQND EIGHIDDRSKP IIL FSMARLDRVKNLTGLVELYGRN		
Consensus	(551) PEIEELIYS ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGRN		
	601		
Sh1	(593) AR LREL VNL VVAGDHGK - ESKDREEQAEFKKMYSHIDEYK LKGHIRWLS		
Sus1	(601) KRLQELVNL VVAGDHGN - PSKDKEQAEFKKMF DLEQYNN LKGHIRWLS		
Sus3	(589) AKIREL VNL VVAGDHGN - PSKDKEQAEFKKMF DLEQYNN LKGHIRWLS		
Consensus	(601) AR LREL VNL VVAGDHG SKDREEQAEFKKMHDLID YNL GHIRWLS		
	651		
Sh1	(642) AQ MN RVRNGELYRYICDTKGAFVQPA F YEA FGLTV VESMT CGLPTIAH		
Sus1	(650) AQ MN RVRNGELYRYICDTKGAFVQPA F YEA FGLTV VESMT CGLPTIAH		
Sus3	(639) AQ MN RVRNGELYRYICDTKGAFVQPA F YEA FGLTV VESMT CGLPTIAH		
Consensus	(651) AQ MN RVRNGELYRYICDTKGAFVQPA F YEA FGLTV VESMT CGLPTIAH		
	701		
Sh1	(692) [REDACTED] VD [REDACTED] L [REDACTED] HSDKTAD [REDACTED] LVN [REDACTED] K KAD S [REDACTED] DE [REDACTED] QG		
Sus1	(700) [REDACTED] VD [REDACTED] L [REDACTED] HSDKTAD [REDACTED] LVN [REDACTED] K KAD S [REDACTED] DE [REDACTED] QG		
Sus3	(689) [REDACTED] VD [REDACTED] L [REDACTED] HSDKTAD [REDACTED] LVN [REDACTED] K KAD S [REDACTED] DE [REDACTED] QG		
Consensus	(701) GGPAEIIIVHGVSFGHIDPYH DKAA LLVDFFDKCKADPSHW ISQGGL		
	751		
Sh1	(742) QRIYEKYTWKLYSERLMLTG VYGFWKYVSNLERRET RRYLEMFYALKYR		
Sus1	(750) QRIYEKYTWKLYSERLMLTG VYGFWKYVSNLERRET RRYLEMFYALKYR		
Sus3	(739) QRIYEKYTWKLYSERLMLTG VYGFWKYVSNLERRET RRYLEMFYALKYR		
Consensus	(751) QRIYEKYTWKLYSERLMLTG VYGFWKYVSNLERRET RRYLEMFYALKYR		
	801	817	
Sh1	(792) SLASQV [REDACTED] SF D-----		
Sus1	(800) PMNSTV [REDACTED] AVE GEPSSK		
Sus3	(789) ELNKTE [REDACTED] ABD-QPQ--		
Consensus	(801) SLASTVPLAID P		

Figure 8b

Figure 9a

		551	600
Sh1	(540)	CTTAACCGACACCTGTCGTCAGTGTGTTCCAGGACAAGGGAGAGTTTGATCA	
Sus1	(520)	CTCAACAGGACACCTGTCATAAAGCTCTTCCATGACAAGGGAGGCAACAA	
Sus3	(458)	CTCAACCGACACTTGTCCTCAATCATGTTCCGCAACAGGGATTGCTTGCA	
Consensus	(551)	CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGGAGGCTTGTAA	
	601		650
Sh1	(590)	CCCCCTGCTGAACCTTCTCAAGGCTCATTAACATAAGGGCACGACCAAGA	
Sus1	(570)	CCCCCTGCTCAACTTCTTCGGCGCCACAACATAACAAAGGGATGACCAAGA	
Sus3	(508)	GCCCCTGTTGGATTTCCTCCGTGGCACCAGGGCACAAAGGGCATGTTATGA	
Consensus	(601)	CCCCCTGCTGAACCTCTCCG GCCCACAACATAACAAAGGGGA GAC ATGAA	
	651		700
Sh1	(640)	TGTTGAATGACAGAACATCCAAGGCCTCGTGGTCTCCAATCATCGCTGAGA	
Sus1	(620)	TGTTGAATGACAGAACATCCGGAGCTTCAGTGTCTGCAAGGTGGCGCTGAGG	
Sus3	(558)	TGCTTAATGATAAAATATAAGCTTGGGAGGGCTTCAGTGTGTGCTGAGCTCC	
Consensus	(651)	TGTTGAATGACAGAACATCCAAGGCCT GTGGTCT CAATCTGCGCTGAG	
	701		750
Sh1	(690)	AAGGCTGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus1	(670)	AAGGCTGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus3	(608)	AAGGCTGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Consensus	(701)	AAGGCTGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
	751		800
Sh1	(740)	GTGCAATGTTCTGAGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus1	(720)	ATTTCTGTTCTGAGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus3	(658)	ATTTCTGTTCTGAGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Consensus	(751)	ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGGTTGGGTGATA	
	801		850
Sh1	(790)	GTGCAAGGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus1	(770)	GCTGTTAGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus3	(708)	CAGGAGGAAGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Consensus	(801)	C GC AAGCGTGTCTGGA AC ATCCACCTCCTTCT GACCTCCTTGAG	
	851		900
Sh1	(840)	GGCGCTGATCTGCGCAATTCAGGTTAGCTGAGGAGGAGCACCTGTC A CT	
Sus1	(820)	GGCGCTGAGATGGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus3	(758)	GGCGCTGAGATGGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Consensus	(851)	GGCCCGAGATCC TCCACCCCTGGAGAAGTTCTTGGAACGATCCCCATGAT	
	901		950
Sh1	(890)	GTTCGAACCTGTTCTGAGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus1	(870)	GTTCGAATCTGCTGAGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Sus3	(808)	TTTTAACGTTCTGAGGAGGAGGAGCACCTGTC A CT CCTGCTGACAC CCATAACTC GA	
Consensus	(901)	GTTCAACGTTGTTATCT TCCCCTCATGG TACTTCGCTAAGCTAATG	
	951		1000
Sh1	(940)	TGCTTGGGATACCCCTGACAGTGGCGCTCAGGTTGTTACATCTGGATCAA	
Sus1	(920)	TCTTGGGTTACCCCTGACAGCGGGAGGCCAGGTTGTTACATCTGGATCAA	
Sus3	(858)	TATTAAGGCTTGGCAGACACAGGGAGGACAGATCGCTATATACTGGACCAA	
Consensus	(951)	T TT GG TACCCCTGACAC GGAGG CAGGTTGCTACAT CTGGATCAA	
	1001		1050
Sh1	(990)	GTCCCGTGTGTTGGAGAATGAGATGCTCTGAGGATTAAGCAGCAAGGCT	
Sus1	(970)	GTGCGCGCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGGCT	
Sus3	(908)	GTCCCGTGCACIAGAAAATGAGATGCTCTCCGTTAAAGAAACAAGGGCT	
Consensus	(1001)	GTCCCGTGTGCT TGGAGAATGAGATGCTCTGAGGAT AAGCAGCAAGG CT	

Figure 9b

		1051	
Sh1	(1040)	TGATATCACTCCGAAGATCCTCATGGTTACCAAGGCTGTGCGCTGAGTG	
Sus1	(1020)	TGACATCACGCCGAAGATCCTTATTGTCACCAAGGTGCGCTGAGTG	
Sus3	(958)	TGATGTTCCCCAAAGATTCTCATGGTTACTCGGCCTGAAAGA	
Consensus	(1051)	TGATATCAC CGGAAGATCCTCATGGTTACCAAGGCTG T CCTGATGCAA	
		1100	
Sh1	(1090)	CTGGGACTACCGTGGTCAGGGCTGAGAAGGTACATGGTAGTGAG	
Sus1	(1070)	CTGGCACCCACCTGGCCAGGGCTGAGAAGGTACATGGAG	
Sus3	(1008)	AAGGAACATCACTGGCAATCGCGGCTGAGAGAAATACGGAGAC	
Consensus	(1101)	CTGG AC AC TGCGGTAGCGGCTTGAGAAGGTACATGG AC GAGCAC	
		1150	
Sh1	(1140)	ACAGACATCACTGGCTGGCTGAGAAGGTACATGGAGAC	
Sus1	(1120)	TGCCATATCCATCGCGTGGCAAGAAGGTACATGGAGAC	
Sus3	(1058)	ACTTACATATCACTGGCTGGCTGAGAAGGTACATGG AAG	
Consensus	(1151)	AC ACATC TTGCGGTTCCCTTCAGAAATGAAATGG ATCCTTCGCAA	
		1200	
Sh1	(1190)	GTGGATCTCGTGTGAGAAGGTACATGGAGAC	
Sus1	(1170)	GTGGATCTCGTGTGAGAAGGTACATGGAGAC	
Sus3	(1108)	ATGGATCTCGTGTGAGAAGGTACATGGAGAC	
Consensus	(1201)	GTGGATCTC CGATTTGATGTCTGGCATACTGGAGACATACACTGAGG	
		1250	
Sh1	(1240)	ATGTTGCAGAAATGAAAGAAGGTACATGGAGAC	
Sus1	(1220)	ATGTTGCAGAAATGAAAGAAGGTACATGGAGAC	
Sus3	(1158)	ATGTTGCAGAAATGAAAGAAGGTACATGGAGAC	
Consensus	(1251)	ATGTTGC GTGAAATTGCTG AGAA T CAGGCCAACCTGACCT ATC	
		1300	
Sh1	(1290)	ATGGAAACTACAGTGTGGAAACCTTGT GCGTCTTGCTCGCACAA	
Sus1	(1270)	ATGGAAACTACAGTGTGGAAACCTTGT GCGTCTTGCTCGCACAA	
Sus3	(1208)	ATGGAAACTACAGTGTGGAAACCTTGT GCGTCTTGCTCGCACAA	
Consensus	(1301)	ATGGAAACTACAGTGTGGAAACCTTGT GCGTCTTGCTCGCACAA	
		1350	
Sh1	(1340)	ATGGGAGTTACTCAGTGTACCTGGCTCATGC CTGGAGAAAAGTAA	
Sus1	(1320)	ATGGGAGTTACTCAGTGTACCTGGCTCATGC CTGGAGAAAAGTAA	
Sus3	(1258)	ATGGGAGTTACTCAGTGTACCTGGCTCATGC CTGGAGAAAAGTAA	
Consensus	(1351)	ATGGGAGTTACTCAGTGTACCTGGCTCATGC CTGGAGAAAAGTAA	
		1400	
Sh1	(1390)	ACCCCAACTCGGACATCAGCTGGCTGAGAAGGTACAGCAGGAGAC	
Sus1	(1370)	ACCCCAACTCGGACATCAGCTGGCTGAGAAGGTACAGCAGGAGAC	
Sus3	(1308)	ATCCAGATTCAGACATAATTGGAGAGAAATTGGATGAGAAGTACACATG	
Consensus	(1401)	ACCC AACTC GACATCTACTGGAGAA TTCGA GA CAGTACCACTTC	
		1450	
Sh1	(1440)	TCTTGCCAGTTCACAGCTGACCTTATTGCCATGAAACACACCGATTTGAT	
Sus1	(1420)	TCTTGCCAGTTCACCACTGACTTGTGATGCCATGAAACACACCGATTTGAT	
Sus3	(1358)	TCTTGCCAGTTCACTGCTGATATAATTGCTATGAAAGAATGCTGATTTTAT	
Consensus	(1451)	TC TGCCAGTCAC GCTGAC T ATTGC ATGAAACATGCCGATTTCAT	
		1500	
Sh1	(1490)	CATCACCAAGCACATTCCAAGAAATGGCGGAAGUAAGGACACCGTGCGG	
Sus1	(1470)	CATCACCAAGCACATTCCAAGAAATGGCGGAAGUAAGGACACCGTGCGG	
Sus3	(1408)	CATCACCAAGCACATTCCAAGAAATGGCGGAAGCAAGGACACCGTGCGG	
Consensus	(1501)	CATCACCAAGCACATTCCAAGAAATCGC GGAGCAAGGACACCGTGCGG	

Figure 9c

		1551	
Sh1	(1540)	AGTACGAGTCCCATATCGCTTCACCTCTCCCTGGCTCTACCGTTCCTG	1600
Sus1	(1520)	AGTACGAGTCACACATGCGTTCAAACTGCCTGGCTCTGTAACCTGCG	
Sus3	(1458)	AGTATGAGAGTCATACTGCCCTTACTCTGCCTGGCTCTGTAACGTTG	
Consensus	(1551)	AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC	
		1601	
Sh1	(1590)	CATGGCATCGATGTTTCGATCCCAGTTCAACATGCTCTGGAGC	
Sus1	(1570)	CACGGCATGATGTTGCAACCCAGCTCAACATGCTCTGGAGC	
Sus3	(1508)	CATGGGATCGATGTTTCGATGCCAACGTTCAACATGCTCTGGAGC	
Consensus	(1601)	CATGGCATCGATGTTTCGATCCCAGTTCAACAT GTCTCTCCTGGAGC	
		1651	
Sh1	(1640)	AGACATGAGTGTCTACTACCGTTCCTGGAAACCGACAGGAGCTAC	1700
Sus1	(1620)	GGACCTGTCATCTACTTCGGCTCTGGAGCTGGAAACGAGCTAC	
Sus3	(1558)	TGACATGTCATTAACGTTTACCTTCGGAAACCGACAGGAGCTAC	
Consensus	(1651)	GACATGTCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT	
		1701	1750
Sh1	(1690)	CGTCGATCTGAAAGCGAGGACAACTCGCTGCTGCTGCTG	
Sus1	(1670)	CGCTGCGCCGGAGGTTGCTGCTGCTGCTGCTGCTG	
Sus3	(1608)	CTGTCGATGTCATGAAATTGCTGCTGCTGCTGCTGCTG	
Consensus	(1701)	CCCTTCATCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C	
		1751	1800
Sh1	(1740)	CGGAGAAGTGGGGCTGCTGCTGCTGCTGCTGCTG	
Sus1	(1720)	CGGAGAAGTGGGGCTGCTGCTGCTGCTGCTGCTG	
Sus3	(1658)	GAAGAAGTGGGGCTGCTGCTGCTGCTGCTGCTG	
Consensus	(1751)	GAGCACAAGTTGTTCTGAA GACAGGAA AAGCC ATCATCTTCTCCAT	
		1801	1850
Sh1	(1790)	GGCGCGCTCTGGACGGCTGCTGCTGCTGCTGCTG	
Sus1	(1770)	GGCTCGCTCTGGACGGCTGCTGCTGCTGCTGCTG	
Sus3	(1708)	GGCAAGACTCGACAGGCTGCTGCTGCTGCTGCTG	
Consensus	(1801)	GGC CGTCTGACCG GTGAGAACATGACAGGGCTGGTCAG TGTCAG	
		1851	1900
Sh1	(1840)	GCAAGAACGGCGCGCTGACGGCTGCTGCTGCTGCTG	
Sus1	(1820)	GGCGAACAAAGGGCTGACGGCTGCTGCTGCTGCTG	
Sus3	(1758)	CTAAAGTCTGCTAAGCTGACGGCTGCTGCTGCTGCTG	
Consensus	(1851)	GCAAGAACGGCGCGCTGAGGGAGCTGGTGAACCTCGTGGTCGTTGCCG	
		1901	1950
Sh1	(1890)	GACCACGG --- CAAGGAGCTGACGGCTGACGGCTG	
Sus1	(1870)	GACCACGG --- CAAGGCTGACGGCTGACGGCTGACGGCTG	
Sus3	(1808)	TACAATGATGTCATAAGCTGACGGCTGACGGCTGACGGCTG	
Consensus	(1901)	GACCACGG CAAC AGTCCAAGGACAGGGAGGAGCAGGCCGAGTTCAA	
		1951	2000
Sh1	(1937)	GAAGATGTACGCCCTATCGACGGCTGACGGCTGACGGCTG	
Sus1	(1917)	GAAGATGTTGACCTCATCGACGGCTGACGGCTGACGGCTG	
Sus3	(1858)	GAAGATGCTGAACTCATCAAGACCCACAACCTGTCGGCTGTCGGCT	
Consensus	(1951)	GAAGATGTATGACCTCATCGAG AGTACAACCTGAACGGCA ATCCGCT	
		2001	2050
Sh1	(1987)	GGATCTCGCGCAGATGAACCGTGTCGGCAACGGGAGGCTGTCGGCT	
Sus1	(1967)	GGATCTCGCCCGAGATGAACCGTGTCGGCAACGGGAGGCTGTCGGCT	
Sus3	(1908)	GGATCTCTGCCAGACAAACAGGGCCGTAACGGGAGGCTGTCGGCT	
Consensus	(2001)	GGATCTC GCCCAGATGAACCG GTCCGCAACGGGAGCTGTACCGCTAC	
		2051	2100
Sh1	(2037)	ATTGCGATACCAAGGGCGATTGTCAGGCTGCTACGAAGCGT	
Sus1	(2017)	ATCTGCGACACCAAGGGCCCTTCGTCAGGCTGCTTCTACGAGGCTT	
Sus3	(1958)	ATCGCTGATACCCATGGTGCTTCTGACAGCCGGCTTGTATGAAGCGTT	
Consensus	(2051)	ATCTGCGATACCAAGGGCGC TTGTCAGGCTGCTG TTCTACGAGCGTT	

Figure 9d

		2101	
Sh1	(2087)	CGGCCTGACTGTGATCGAGTTCATGACGTGGGTCTGCCAAGGAAAGC	2150
Sus1	(2067)	CGGGCTGACGGTGGTTGAGGCCATGACCTGGGCTGCCAACGTTGGCN	
Sus3	(2008)	CGGTCTCACCGTCTGGTGGGCCATGACCTGGGTGGCTTCTT	
Consensus	(2101)	CGG CTGAC GTGGTGAGGCCATGACCTGGG CTGCC ACGTTCGGA	
		2151	2200
Sh1	(2137)	CCTGCCATGGCGGCCCTGCTGACATGATGGTGGACGGGATACTGCCCTG	
Sus1	(2117)	CCGCCTACGGCGGTCCGCCAGATGGTGGTGGACGCCCTGCTGAGCTTAC	
Sus3	(2058)	CGCTCCATGGAGTCCACCTGACATGATGACCTGGCTTCTGGCTTC	
Consensus	(2151)	CC CCATGGCGGTCC GCTGAGATCATCGTCACGGCGT TCTGGCTTC	
		2201	2250
Sh1	(2187)	CACATTGACCCCTTACCAACAGCGAGAAGGCCGGGATACTGCCCTGAG	
Sus1	(2167)	CACATGACCCCTTACCAAGGCCAGAAGGCCGGTGGCCCTGCCCTGAG	
Sus3	(2108)	CACATTGACCCGTAACCAACCCCGAACAGGCTGTTAACGCACTGCC	
Consensus	(2201)	CACATTGACCCCTTACCAACGACAAGGC GCGGATCTGCTGGTCGACTT	
		2251	2300
Sh1	(2237)	[REDACTED]TACGAAATGGAAAGGAGCTTAAGTTGAGTCTGAG[A]G[A]A	
Sus1	(2217)	[REDACTED]TACGAAATGGAAAGGAGCTTAAGTTGAGTCTGAG[A]G[C]	
Sus3	(2158)	[REDACTED]TACGAAATGGAAAGGAGCTTAAGTTGAGTCTGAG[A]G[TGGA]	
Consensus	(2251)	CTTCGACAAGTGAAGCAGA CCGAGCCACTGGG CAAGATCTC CAGG	
		2301	2350
Sh1	(2287)	[REDACTED]CTGAGAGAGATTT[G]C[C]C	
Sus1	(2267)	[REDACTED]CTGAGAGAGATTT[G]C[C]G	
Sus3	(2208)	[REDACTED]CTGAGAGAGATTT[G]C[C]A[A]A[A]A	
Consensus	(2301)	GGGGCTGAGCG AT TA GAGAAGTACACCTGGAAAGCT TACTC GAG	
		2351	2400
Sh1	(2337)	[REDACTED]GATGAGCCGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAG	
Sus1	(2317)	[REDACTED]GATGAGCCGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAG	
Sus3	(2258)	[REDACTED]GATGAGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAG	
Consensus	(2351)	AGGCTGATGACCTGACCGGGCTGTACGGTTCTGGAAGTACGTGTCAA	
		2401	2450
Sh1	(2387)	[REDACTED]GAGAGGGGGGGAGAGCCGCGGAA[A]C[C]C	
Sus1	(2367)	[REDACTED]GAGAGGGGGGGAGAGCCGCGGAA[G]G[C]G[G]C	
Sus3	(2308)	[REDACTED]GAGAGGGGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	
Consensus	(2401)	CCTGGAGAGGGCGAGACCCGGCGTACCT GAGATGTTCTACGC CTGA	
		2451	2500
Sh1	(2437)	[REDACTED]TACCGTAGCCCTGGAAAGCAGGTTGGCTTCTT[C]-----TT[G]	
Sus1	(2417)	[REDACTED]TACCGGACCACTGGGAGGACGGTGGCTGGGAGGAGGAGGAGGAG	
Sus3	(2358)	[REDACTED]AGTCCGGAGCTGGCGAAGACCGTGGCTTCAAT[G]CCAACCGCG	
Consensus	(2451)	AGTACCGCA CCTGGCGAGCACCGTGGCTGGCC T GA G AG	
		2501	2550
Sh1	(2481)	[REDACTED]ACGGGAAAGAAGGAGA-A[G]AAGAAGAAGAAGCCTGGGG[G]A-----[G]	
Sus1	(2461)	[REDACTED]GAGCCCTCCAGCAACTGAGTGGCGTACGGCGCCACAGAATGTC-----[G]	
Sus3	(2408)	[REDACTED]TAGCTTGGCGAACCTGGCAACTGGTACGACTTGGTACAGAATGTCACCT[G]	
Consensus	(2501)	TAGC GC AGAA G GA TGCGTAACA GGCACAGGCCTGA G	
		2551	2600
Sh1	(2525)	[REDACTED]ACCATCGCCTGCATTTGATCT-----[G]T-T[G]A[CCGCAATGGG	
Sus1	(2507)	[REDACTED]ATCGATGAGCGAGAGGGAGGACTGGG-----[G]T-GTGGTGT[G]T[G]C	
Sus3	(2458)	[REDACTED]AAGGACCTTCAGTAATTAGGCGGGCAGACGGTACCGAATAAAT[G]T[G]	
Consensus	(2551)	AACGATC C G A TT G CTCGG GT GTCA CAATTCGC	

Figure 9e

	2601	
Sh1	(2565) AATGTTAGTCGTCTATTGGAGTTATGTG--TACTTCTTTCGCAGAGCT	2650
Sus1	(2551) TTGCCATTCTCTTCCTTCCTTCTCC--TTCGGCGAGGGAAATAA	
Sus3	(2508) CGGAGCTGAACCTGGTTTCTATTATGTACATAAGCCTATC	
Consensus	(2601) TG TGTC TG TTT TT TTATGT TACT GGAGTC AA AAAAT	
	2651	2700
Sh1	(2613) TCGCTCCATTCTCGTTTCTTCCCTTCCTTGAGEGTTGGAGGCCG	
Sus1	(2599) AGACTC-TGCTT-TCGCTAGGEGGCCGCTTGAGCTTCTT	
Sus3	(2558) TACTGAAGGAGGTGGGTTGCAGTCTGTCTTGAGCT	
Consensus	(2651) TG TTC TGCT GTTG TTG CGTTGTGTTCGTT CTG C GCT	
	2701	2750
Sh1	(2663) GCCTGGTCTCTAGTATGGTGGGAATTGGCTGCACCTTGTTCAAA	
Sus1	(2647) CAGAGCTAAATTTACCTACCG--TTGCTAAAGGTGCGCACTTG	
Sus3	(2600) TCGTGTAACTGCTAACAGCTGTC--GGCTGCATTCCTGCTGG--C	
Consensus	(2701) ACTGGTT ATATTAAGCTG C TTGGCTGCA CTT TTC TGA T A	
	2751	2800
Sh1	(2713) AATCTCTTGTCCTCTTCCCTGGC--	
Sus1	(2695) TCGCTGTTGCTAGTACCTACCGCTAGCTAGCTCGTTG	
Sus3	(2644) TGCCTAAAGAAGGTGAAATACAACATCTTGTGAC	
Consensus	(2751) A C GC GGC CTTGTA GTCTGATAGA TG T TA T TG C	
	2801	2850
Sh1	(2747) -----	
Sus1	(2745) GTCTGTTGGGGCGTTGGTGGTGGTGTCTTCAAGTAGGGCGT	
Sus3	(2694) TGTAAAAAAATAAAAAATAAAAAAAAAAAAAGCAGCCG-----	
Consensus	(2801) G A A AA G G G C	
	2851	2900
Sh1	(2747) -----	
Sus1	(2795) GGTGCTCCCTTGTTCCTGGATGGATGTTGCTCCTGAATAATAATCG	
Sus3	(2738) -----	
Consensus	(2851) -----	
	2901	2950
Sh1	(2747) -----	
Sus1	(2845) TAGTGGCCTGGAGCCCTTCTGAAATAAGAGCAGCATCCTAGTGCTT	
Sus3	(2738) -----	
Consensus	(2901) -----	
	2951 2964	
Sh1	(2747) -----	
Sus1	(2895) ACCTTTGCAGCTGT	
Sus3	(2738) -----	
Consensus	(2951) -----	

Figure 9f

CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGGCCGGGTAGGAG
CGCGCGCGCGCGCGGAACGACCCACCGGTGGCGCAGCCATGTCTGCCCCGAAGCTGA
ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCCTCCACGCGCACCGAACGAGC
TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGAAAGGGATCCTGCAGCCGCACCACA
TCCTCGACCGCCTCGACGAGGTCCAGGGCTCCGGGTCCGCGCTCGCCGAGGGACCCT
TCCTCGACGTCCCTCCGCTCCGCGAGGAGGCGATCGTGTGCCGCCG

Figure 10

Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11

ATGCTGCCCGAAGCTGAACCGCAACGGAGCATCCGG

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

[REDACTED]	accgcgtcga	ggacacccctc	cacgcgcacc	gcaacgagct	60
cgtcgccctc	ctgtccaagt	acgtgaacaa	ggggaaaggc	atccctgcagc	120
cctcgacgcg	ctcgacgagg	tccagggtc	cgggggccgc	gegctagccg	180
cctcgacgtc	ctccgctccg	cgcaggagc	gatctgtctg	ccgcccgtcg	240
ggtgcgcccc	cgcggggag	tttggagta	cgtccgcgtc	aacgttcacg	300
cgagcagctc	acagtctcg	agtaacctcg	cttcaaggag	gagttgtcg	360
caatgatccc	tacgttctcg	agcttgactt	cgagccgtc	aatgtctcg	420
aaatccgtca	tcatctattt	gaaacggtgt	gcagttcctc	aaccgacat	480
catgtccgc	aacaggattt	gcttggagcc	cctgttggat	ttcctccgtg	540
caaggggcat	gttatgatgc	ttaatgatag	aatacaaagc	ttggggaggc	600
gctgacaaa	gtcgaggagc	acttgtcaaa	gtccctgtc	gacacaccat	660
tgcttataaa	tttcaagagt	ggggccttgg	gaaaggttgg	ggtgatacag	720
tttggaaatg	atccatctcc	ttcttagacat	cattcaggcg	ccagacccat	780
gaaattcttg	gggaggatcc	ccatgatttt	taacgttgtt	gtggtatccc	840
ctttggtaa	gctaattgtat	taggcttgc	agacacagga	ggacagatcg	900
ggaccaagtc	cgtgcactag	aaaatgagat	ggttctccgt	ttaaagaaaac	960
tgtttccca	aaggattctc	ttgttactcg	gctgatacc	gatcggaaag	1020
caatcagcgg	cttggagagaa	tttagtggaaac	acagcatact	tatcattttac	1080
cagaatgaa	aatgggatac	ttaagaatag	gatataaga	tttgatgtgt	1140
ggaacattt	gtcgaggatg	ctgcttggta	aattgtctgt	gaattacaag	1200
cttcataatt	ggaaactaca	gtgtggaaa	tcttggcg	tcattgttat	1260
gggaattacc	cagtgcacaa	ttgctcatgc	tctggaaaag	actaagtatc	1320
catatttgg	aagaatttcg	atgagaagta	ccatttctcc	tgccagttca	1380
aattgtctg	aacaatgtc	attttatcat	caccagcaca	taccaagaaa	1440
caaaaaact	gttggacagt	atgagagtc	tactgtctt	actctgtctg	1500
agttgtccat	gggatcgtat	tcttcgatcc	aaagtccat	atagtcttc	1560
catgtccata	tactttccac	ataccggagaa	ggccaagcga	ctcacctctc	1620
aatcgaaaat	ttgatattatg	acccggagca	aaacgtatgaa	cacattgggc	1680
ccggtaaag	cccatccctc	tctccatggc	aaagactcgac	agggtaaga	1740
gctgtcgaa	gcttttcta	agtgcgtaa	gctgagggag	ctggtaaacc	1800
tgccgggtac	aatgtatgtca	acaagtccaa	ggacagggaa	gagatcgcgg	1860
gatgtcatgaa	ctcatcaaga	ccccacaactt	gttcgggcag	tctctgttgc	1920
gacaaacagg	gcccgtaaacg	gcgagctca	tcgctacatc	gctgatacc	1980
cgtacagccg	gctttgtatg	aaggcttgg	tctcaccgtc	gttgaggcc	2040
gcttcctact	ttcgcgacgc	tccatggagg	tccagctgag	atggcgtctc	2100
gggcttccac	attgaccctg	accaccccg	acaggctgtt	aatctgtatgg	2160
cgaccgggtc	aagcaagacc	cagatcactg	ggtgaatata	tctggagcag	2220
catatacgg	aagtacacat	ggaagatata	ctcagagagg	ttgtatgacac	2280
ctacggttc	tgaagttacg	tgtcgaagct	cgagaggctg	gagacgaggc	2340
gatgttctac	atactgtatg	tccgcgact	ggcgaagacc	gtggccgttg	2400
accgcgttag	tttgcgcaac	tgcgactcg	tagcacttgg	tacaagactg	2460
gacctttagt	aatttaggcg	cggcagacgg	tagccataaa	aatgtgccgg	2520
gttttttatt	atgtacataa	tggcgtata	acaaaattac	tgaaggcagg	2580
tttgtgttgc	gttactgttt	actgttattat	gtcaagctgt	cggtctgcaat	2640
gcaagccgca	ggcactggtg	aagtgtctgt	aaatacatca	tattctgttg	2700
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaagg	cgcccg		

Figure 11